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Metagenomic analysis of foaming in biogas reactors

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Foaming is one of the major problems that occasionally occurring in biogas plants affecting negatively the overall anaerobic digestion (AD) process. According to a recent survey, 15 out of 16 full-scale biogas plants, which were surveyed in Denmark, faced foaming incidents in the main reactor and/or in the pre-storage feeding tank, resulting in 30-50% biogas production loss. The main causes of foaming in biogas plants fed with agricultural and industrial wastes are organic overloading, feed-

stock composition and operational parameters. However, the contribution of specific microorganisms on foam generation in this AD system has not been previously investigated. The aim of the present study was to define potential correlation between specific microorganisms and foaming in manure based biogas reactors overloaded by different feedstock composition (i.e. proteins, lipids and carbohydrates).

The experiment was carried out in three continuous stirred tank reactors (CSTR) denoted as R1, R2 and R3. The total and the working volume of each reactor was 2 and 1.5 L, respectively. Each reactor was continuously stirred using a magnetic stirrer. The operating temperature was maintained at 54 ± 1 °C using thermal jackets. Each reactor was fed with a different mixed substrate, which was found to have an influence on foam formation in our previous study. Thus, the influent manure was supplemented with gelatine as a representative of proteins (R1), Na-Oleate as a representative of lipids (R2) and glucose as a representative of carbohydrates (R3). The hydraulic retention time (HRT) of all reactors was kept constant at 15 days. The whole experiment was divided into two periods. During the first period, the reactors were fed only with cattle manure. Once steady state conditions were reached, liquid sample from all reactors was obtained for DNA extraction and metagenomic analysis. After sampling, the feedstock composition of each reactor was changed by the addition of gelatine or Na-Oleate or glucose (second experimental period). As a consequence, foam formation was observed in all reactors approximately after one HRT period. Once the daily volume of the formed foam was steady, samples were taken again for DNA extraction and metagenomic analysis. Data derived from the 16S rDNA sequencing were compared in order to determine differences in the microbial consortium of the reactors prior and after foaming.

The results obtained from the present study revealed that significant variations in the microbiology of the manure-based biogas reactors were observed after foam formation. A number of genera could be linked to foaming as they produce biosurfactants (Lactobacillus, Bacillus, Pseudomonas, Thermotoga), others contain mycolic acid in their cell wall (Thermoactinomyces, Pseudonocardia) or decrease the surface tension of the media (Micrococcus, Streptococcus). Frankia, Dialister and Paenibacillus are known to be correlated to this phenomenon but their mechanism is still unclear. The results from the present study reinforce the idea that a microbial abundance threshold is critical for foam formation.